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Soil stabilisation for DNA metabarcoding of plants and fungi. Implications for sampling at remote locations or via third-parties

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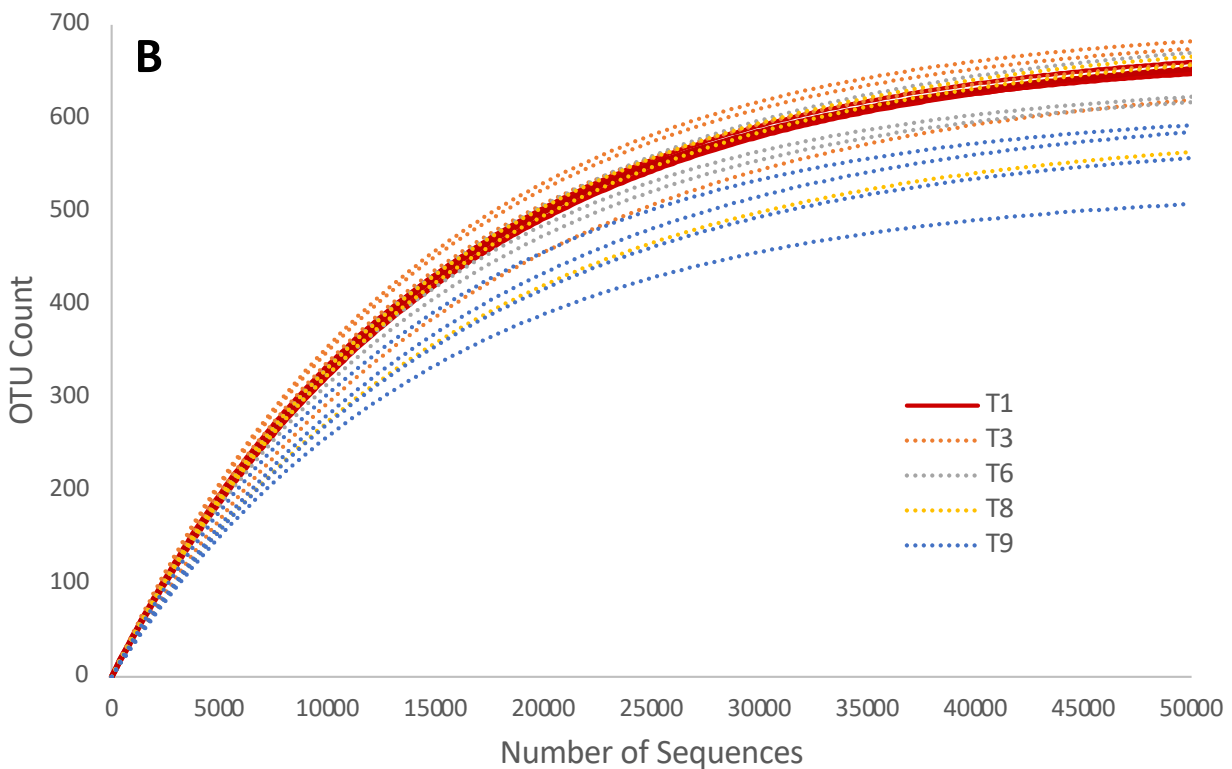
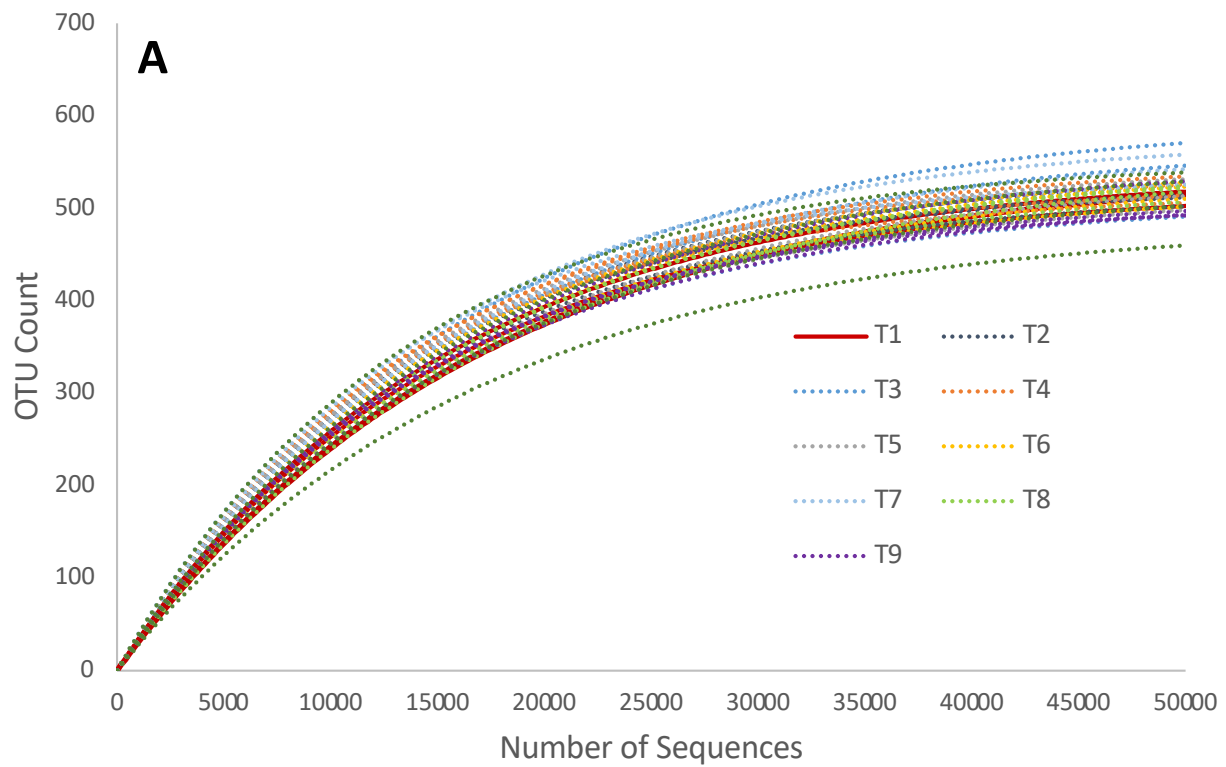
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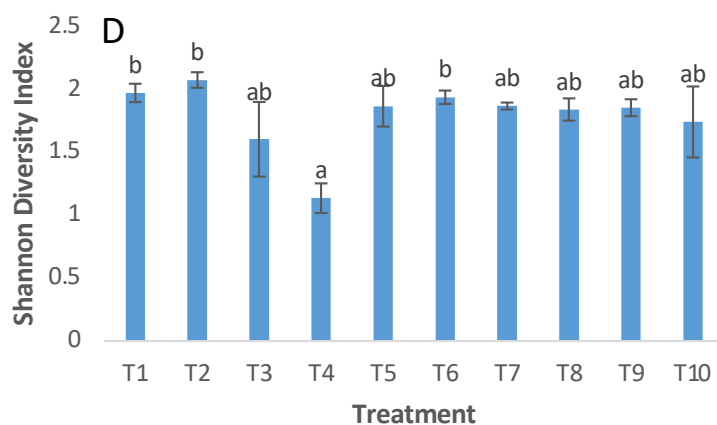
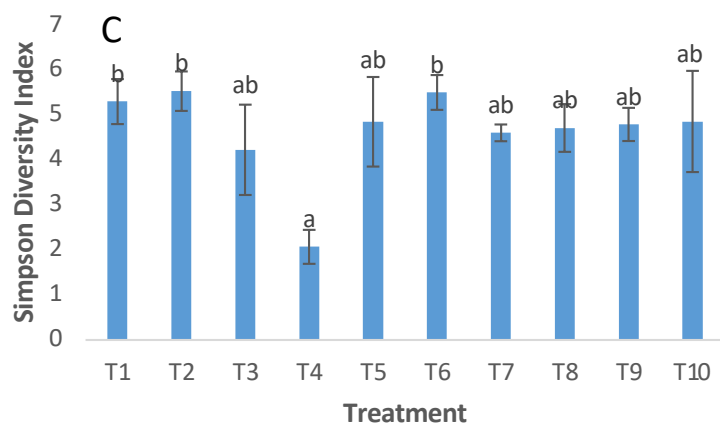
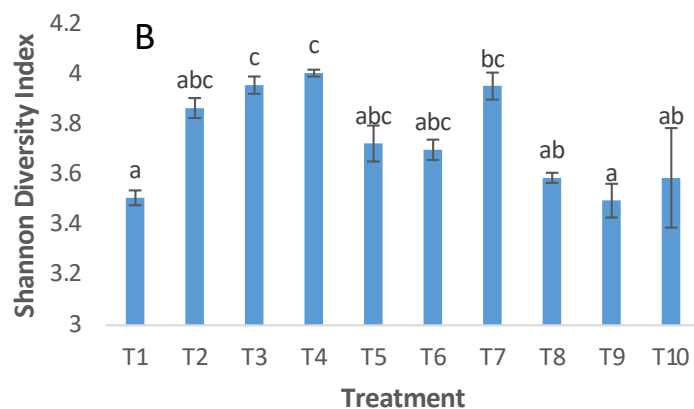
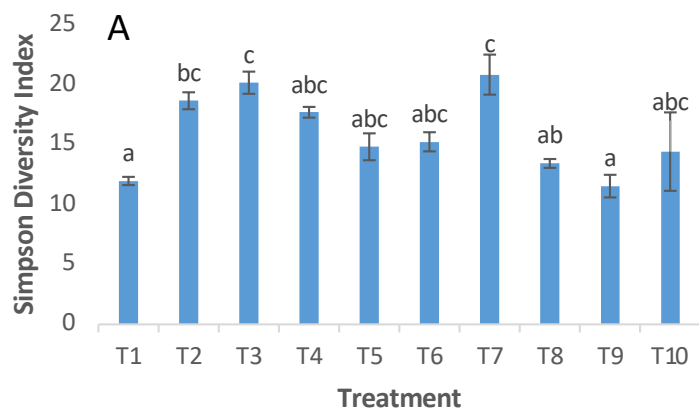
SuppData 1. Photo of the hairdrier apparatus used for active air-drying of soil (treatment T5)

SuppData 2. Fungal forward primer sequences with target group to amplify all fungal groups, and also Stramenopiles (Ooomyces) devised by Tedersoo et al. (2014)

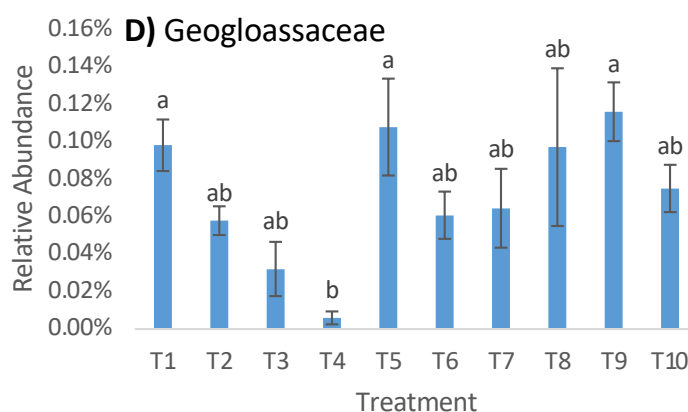
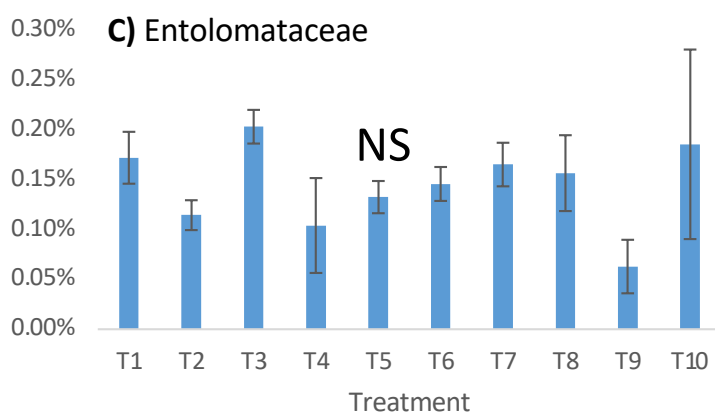
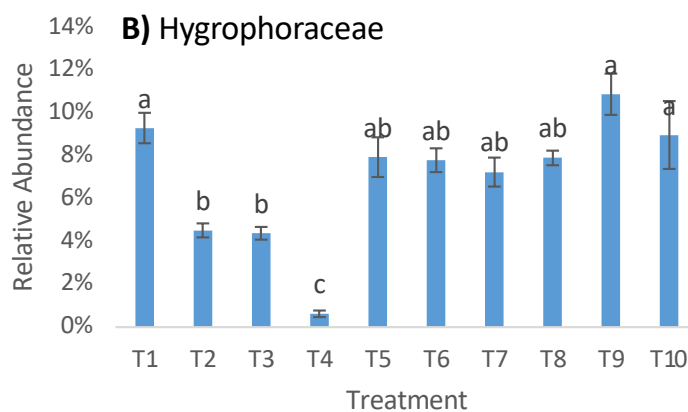
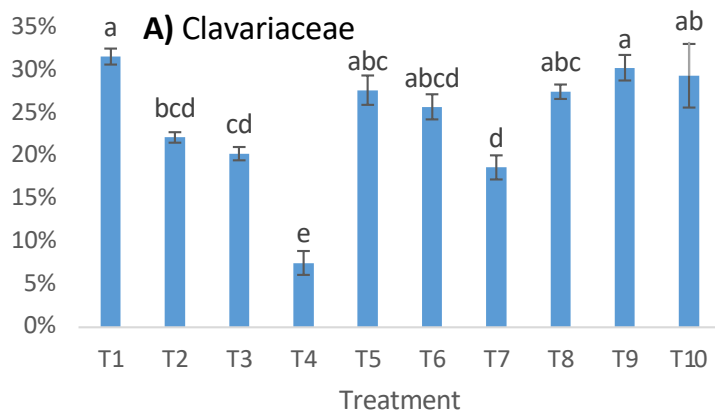
Name	Sequence	Target Group
ITS3NGS1	CTAGACTCGTCATCGATGAAGAACGCAG	Ca. 95% of all fungi
ITS3NGS2	CTAGACTCGTCAACGATGAAGAACGCAG	Chytridiomycota
ITS3NGS3	CTAGACTCGTCACCGATGAAGAACGCAG	Sebacinales p.parte
ITS3NGS4	CTAGACTCGTCATCGATGAAGAACGTAG	Glomeromycota
ITS3NGS5	CTAGACTCGTCATCGATGAAGAACGTGG	Sordariales p.parte
ITS3NGS10	CTAGACTCGTCATCGATGAAGAACGCTG	Stramenopila



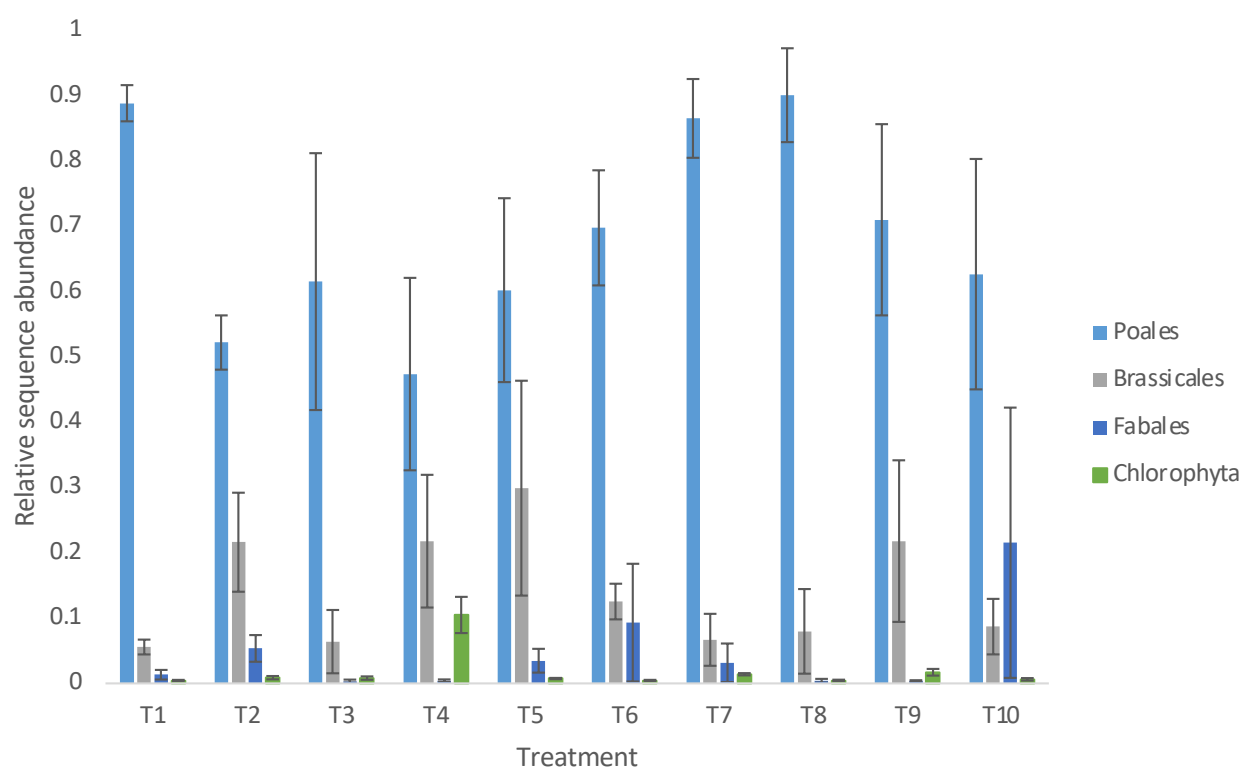
SuppData 3. Rarefaction curves of A) Brigniant soil and B) Gogerddan soil, generated through random sampling of sequences using Mothur. Curves show increased spread of OTU counts of treated soils compared to control T1 and indicate a sufficient sequencing depth at the lowest cut-off (52 931 for Brigniant; 44 864 for Gogerddan).



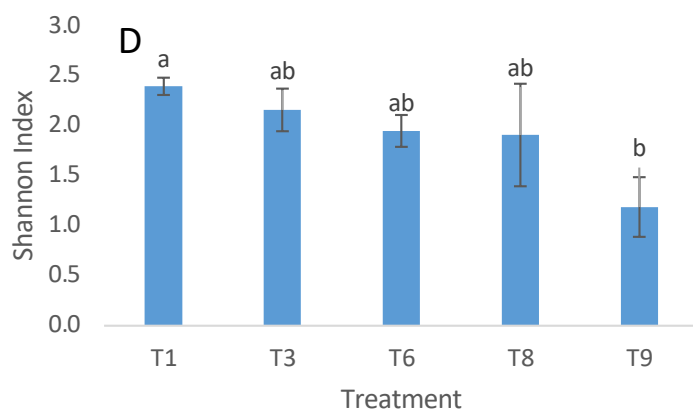
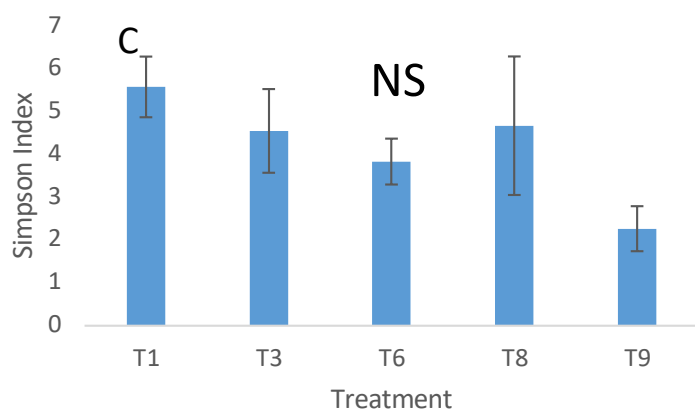
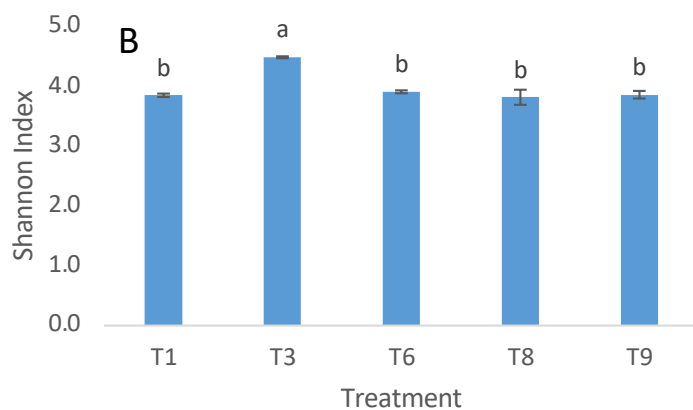
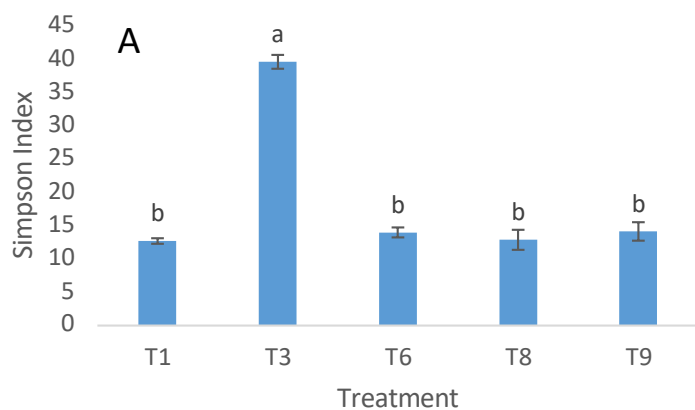
SuppData 4. Variations in diversity indices by storage treatment for the upland (Brignant) soil A) Fungi Simpson diversity index B) Fungi Shannon diversity index. C) Plant Simpson diversity index D) Plant Shannon diversity index (n=4). Letters above the bars indicate significant groupings as determined by Tukey's HSD post hoc test and error bars show standard error of the mean.



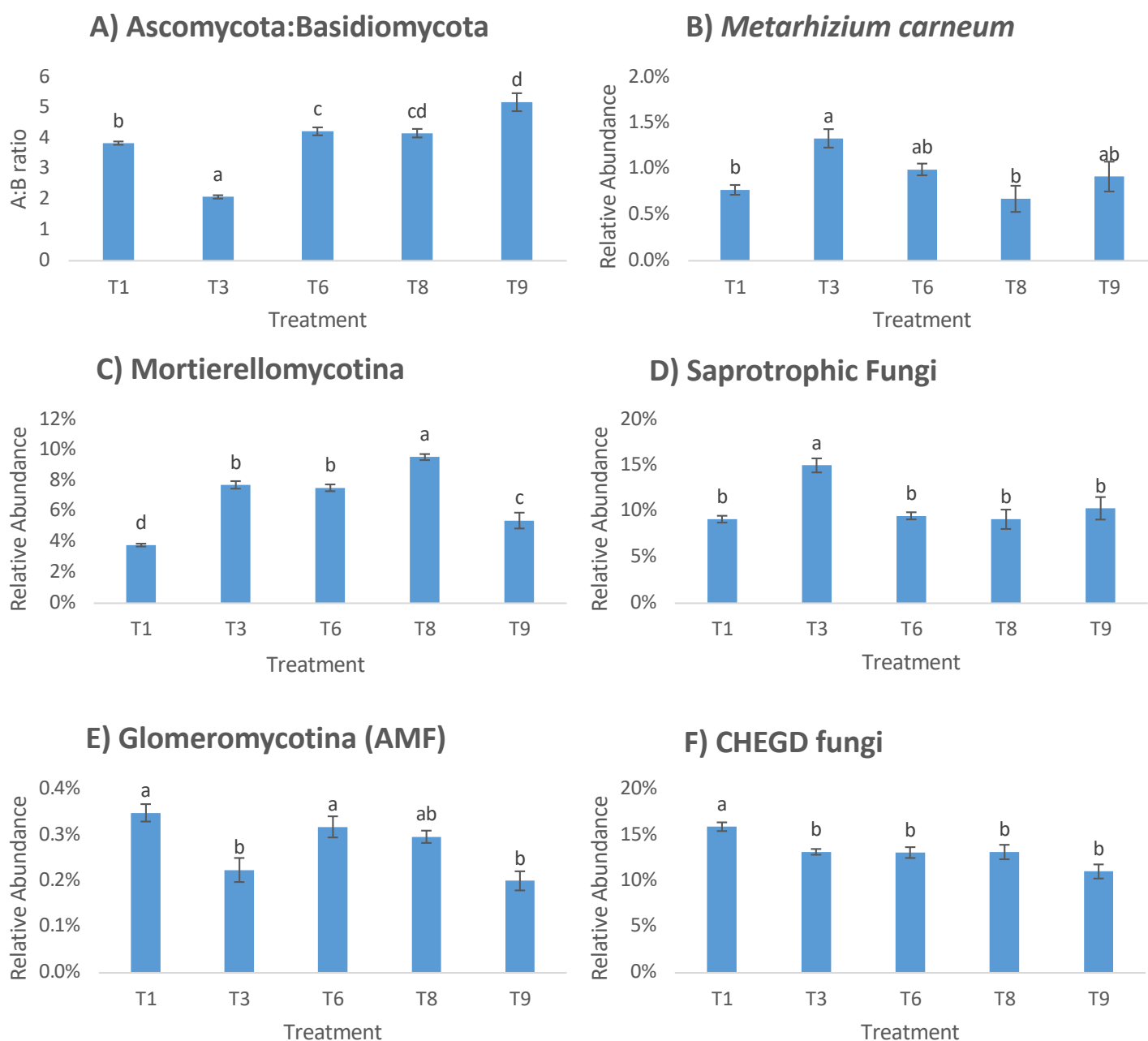
SuppData 5. Relative abundance of CHEG fungi by storage treatment for (Brignant soil). A) Clavariaceae; B) Hygrophoraceae; C) Entolomataceae; D) Geoglossaceae (n=4). Letters above the bars indicate significant groupings as determined by Tukey's HSD post hoc test and error bars show standard error of the mean. NS indicates no significant treatment effect.



Suppdata 6. Relative sequence abundance of most abundant plant orders and Chlorophyta (Brignant soil) (n=4). Error bars show standard error of the mean.



SuppData 7. Variations in diversity indices by storage treatment for the alluvial (Gogerddan) soil A) Fungi Simpson diversity index B) Fungi Shannon diversity index. C) Plant Simpson diversity index D) Plant Shannon diversity index (n=4). Letters above the bars indicate significant groupings as determined by Tukey's HSD post hoc test and error bars show standard error of the mean. NS indicates no significant treatment effect.



SuppData 8. Relative abundance of fungal groups by storage treatment for the alluvial soil (Gogerddan) A) Ascomycota to Basidiomycota ratio; B) *Metarhizium carneum*; C) Mortierellomycota; D) Saprotrophic fungi; E) Glomeromycotina (Arbuscular mycorrhizal fungi); F) Grassland fungi (CHEGD) (n=4). Letters above the bars indicate significant groupings as determined by Tukey's HSD post hoc test and error bars show standard error of the mean.